

The Challenge of Incorporating Regulatory Effect in Genome-scale Networks

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Genomic and bibliomic data has been used to reconstruct a number of genome-scale metabolic networks. The stoichiometric structure of these networks has enabled a series of basic and applied studies that address both proximal and distal causation in biology. One of the challenges going forward with computational models at the genome-scale is to account for regulatory effects. Regulation of metabolic enzymes occurs primarily at two levels; 1) the transcriptional level, and 2) the post-transcriptional (protein expression and activity) level. Significant progress is being made with characterizing, reconstructing and modeling transcriptional regulatory networks regulating metabolism. However, the development of the corresponding methods for incorporating post-transcriptional regulation into genome-scale models is still at an early stage. The current state and future challenges of incorporating both transcriptional and post-transcriptional regulation in genome-scale networks will be discussed.